

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Zabeau, Marc  
Vos, Pieter  
Simons, Guus
- (ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SPENCER & FRANK
  - (B) STREET: 1100 New York Avenue, N.W., Suite 300 East
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/EP96/03480
  - (B) FILING DATE: 06-AUG-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: EP 95401849.5
  - (B) FILING DATE: 07-AUG-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Gollin, Michael A.
  - (B) REGISTRATION NUMBER: 31,957
  - (C) REFERENCE/DOCKET NUMBER: GUPLA 0008
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-414-4000
  - (B) TELEFAX: 202-414-4040

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTGCGTAC CAATTCNNN

19

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATGAGTCCT GAGTAANNN

19

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGTAGACT GCGTACC

17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTGGTACG CAGTCTAC

18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGATGAGT CCTGAG

16

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACTCAGGAC TCAT

14

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACTGCGTAC CAATTC

16

- (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATGAGTCCT GAGTAA

16

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTGCGTAC CAATTCAGA

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATGAGTCCT GAGTAATCT

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1798..5595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAAAAAGCAG	CTTTAAAAAA	AGTACTTTKG	AAAGGKGCTG	AAACTTATTT	TTTGAAATAA	60
GCAGTTATGT	GTTTGGAAWA	AAAGTGCTGA	AGTTGCTATG	TCAAACATGA	AAAGGGRAAA	120
AATGGAAGAA	AGAGWTGTTA	GGGTTATGTC	GTAATTTGGA	GATTGTATAA	AAATATTAAG	180
GGCAAAAAAA	ATAAAAAATGT	GTCAACTTAA	AACAGCTTAT	AAGCTAAAAG	TTAAAAGCTG	240
GGGTAGAGGT	GTTTTTTTTT	TTTTTAGCTT	ATAAGTTGTT	TTAAGTTGAC	CACATTTTTA	300
TTTTTKTTGC	CCTTAATATT	TTTATACAAT	CTCAAAATTA	CGACATAACC	CTAACATCTT	360
TTTCTCCCAT	TTTTTCCTTT	TCACGTTTGA	CATAGCAACT	TCAGCACTTT	TATCCAAACA	420
CATAACTGCT	TATTTTAAAA	ATAAGTTTCA	GCACTTTCAA	AAGTACTTTT	TTAAAGCTGC	480
TTTTATTAAG	CCCATCCAAA	CGGGCCCTAA	AATTGCTAAT	GTTTGCTCTT	TCTATTCTCA	540
AACTCCGTAA	TATTTAAGAA	AATTGCTAA	TGATAGGTCA	CTTTTAACAC	TAAATAATTA	600
TAAATTGGGT	AGAAATTTAT	TTATCATTTT	AAGCTTTTTT	AATTTTGAGT	CTTCTCCCTA	660
ATTAAGACCC	TTCCCCTCTT	GCTTCAATTA	TTTAACTGAA	TAGTCTTTGT	CTTATTGTTG	720
GGTGAAAGTC	TGTCTTCTTG	TTAGGTACTA	AGTCCTACAA	TAATATCAAT	AATTGCTAT	780
GGAGAAAAAA	ATATTATAGG	AGAAAAATAA	TTAATTTTAA	TTCATGAATA	TGTCTTAATA	840
TGCAACTCAT	TTTGCTTATA	TATATCAAAT	TAAACTCTGT	TCCTTTAACT	TTTTCCTATG	900
AAGATACATT	TTAATTTATT	TGATGAGGTT	AGTTTTGAAA	TTTATATTAT	AATAATGAAA	960
TGATATAACT	TAAAAGAAGT	TGTTTGATAT	CTTATCAGAA	TCATGCAGGT	ACTCATAATA	1020
TAAGAAATAA	TTATGATGAA	ATTTATATAT	GTTTTATGCA	GAGATTTATT	ACGCATTGTT	1080
TACTTGGGTT	ATGTATTACT	TATTTCATCT	TTTATCAGAA	TGTAAAATTA	TCATTCAATA	1140
AGAAATCCAA	TTCTGTTAAA	TTCAAAATAC	AAACAATAAC	ATTTTCAAGA	CCGATTTTTT	1200
GCCCAAGAAT	ATACAGTAAA	CATATTTATG	ATATGGTAGG	TCTCTTTAGT	AATTGACCAA	1260
CAAGGATTGT	GGTGGAGTGG	GAAATACTCT	TTAATACTTC	ACCAAGAGGT	CTCCAATTTG	1320
AGCCCCTGAA	TACGAAATCG	TCTTTGTTAG	TATATACCCT	AACCTAATAC	AAAAATTAGT	1380
ATATTAGCCT	TNACAGCTAA	AATCTTTGTG	ACCTGTAAGT	CACGCGAGGA	CAAAATTTACC	1440
GTAACACCAA	CTTATTCATG	ATATAATTGT	CCCTTTTAGC	ACGGTAATAA	TGAGGTGGGT	1500
AGAAATTTAT	TACTTGAGGG	CCCTTTCTAC	ACCCACCCTT	ATTCTCTTGC	TTCAATTATT	1560
GAATTGAAGA	AGTAATGAAA	AAACAGACTC	CATTGGATAA	AGGACAGTTT	GCAAACACAG	1620
CTGTAACAAT	TTAGAGCACT	AGCAAAATAG	AGAGAGTTTT	GAGAGAAATT	TTTGTTTGCA	1680
AATTACTCTT	AACCTTCAGC	AGGTAAAATA	AAGTTCTTAA	CTGAGACTAT	TTGAAGATAT	1740
ATTTTGTTAA	AGAATCATTT	TGTGTGTTTC	CTTGTTTTGC	TTTTGCAGAT	TTGAGAA	1797

ATG Met 1	GAG Glu	ATT Ile	GGC Gly	TTA Leu	GCA Ala	GTT Val	GGT Gly	GGT Gly	GCA Ala	TTT Phe	CTC Leu	TCC Ser	TCA Ser	GCT Ala	TTG Leu	1845
				5					10					15		
AAT Asn	GTT Val	CTG Leu	TTT Phe	GAT Asp	AGG Arg	CTT Leu	GCT Ala	CCT Pro	AAC Asn	GGT Gly	GAT Asp	CTG Leu	CTC Leu	AAC Asn	ATG Met	1893
			20					25					30			
TTT Phe	CGG Arg	AAG Lys	CAT His	AAG Lys	GAT Asp	CAT His	GTT Val	AAG Lys	CTC Leu	TTA Leu	AAG Lys	AAG Lys	CTG Leu	AAA Lys	ATG Met	1941
		35					40					45				
ACT Thr	TTG Leu	CGT Arg	GGT Gly	ATT Ile	CAG Gln	ATT Ile	GTG Val	CTA Leu	AGT Ser	GAT Asp	GCA Ala	GAG Glu	AAT Asn	AAG Lys	CAA Gln	1989
	50					55					60					
GCA Ala	TCA Ser	AAT Asn	CCA Pro	TCT Ser	GTG Val	AGA Arg	GAC Asp	TGG Trp	CTT Leu	AAT Asn	GAG Glu	CTT Leu	CGA Arg	GAT Asp	GCT Ala	2037
	65				70				75						80	
GTC Val	GAC Asp	TCT Ser	GCT Ala	GAA Glu	AAT Asn	TTA Leu	ATA Ile	GAA Glu	GAA Glu	GTC Val	AAT Asn	TAT Tyr	GAA Glu	GCT Ala	TTG Leu	2085
				85				90						95		
AGG Arg	CTT Leu	AAG Lys	GTG Val	GAA Glu	GGT Gly	CAG Gln	CAT His	CAG Gln	AAT Asn	TTT Phe	TCA Ser	GAA Glu	ACA Thr	AGC Ser	AAC Asn	2133
			100					105					110			
CAG Gln	CAA Gln	GTA Val	AGT Ser	GAT Asp	GAT Asp	TTT Phe	TTC Phe	CTT Leu	AAC Asn	ATA Ile	AAG Lys	GAC Asp	AAG Lys	CTG Leu	GAA Glu	2181
		115					120					125				
GAC Asp	ACT Thr	ATT Ile	GAA Glu	ACA Thr	TTA Leu	AAG Lys	GAT Asp	TTG Leu	CAA Gln	GAG Glu	CAA Gln	ATT Ile	GGT Gly	CTC Leu	CTT Leu	2229
	130					135					140					
GGC Gly	TTA Leu	AAG Lys	GAG Glu	TAT Tyr	TTT Phe	GAT Asp	TCC Ser	ACG Thr	AAA Lys	CTA Leu	GAA Glu	ACT Thr	AGA Arg	AGA Arg	CCT Pro	2277
	145				150					155					160	
TCA Ser	ACT Thr	TCT Ser	GTG Val	GAT Asp	GAT Asp	GAA Glu	TCT Ser	GAT Asp	ATC Ile	TTT Phe	GGT Gly	AGG Arg	CAG Gln	AGC Ser	GAA Glu	2325
				165				170					175			
ATA Ile	GAG Glu	GAT Asp	TTG Leu	ATT Ile	GAC Asp	CGT Arg	CTA Leu	TTG Leu	TCT Ser	GAA Glu	GGT Gly	GCA Ala	AGT Ser	GGG Gly	AAA Lys	2373
			180					185					190			
AAG Lys	CTG Leu	ACA Thr	GTA Val	GTT Val	CCT Pro	ATC Ile	GTT Val	GGA Gly	ATG Met	GGC Gly	GGC Gly	CAG Gln	GGC Gly	AAG Lys	ACA Thr	2421
		195				200						205				
ACA Thr	CTT Leu	GCT Ala	AAA Lys	GCC Ala	GTA Val	TAC Tyr	AAT Asn	GAT Asp	GAG Glu	AGG Arg	GTG Val	AAG Lys	AAT Asn	CAT His	TTT Phe	2469
	210					215					220					
GAT Asp	TTG Leu	AAA Lys	GCG Ala	TGG Trp	TAT Tyr	TGC Cys	GTT Val	TCT Ser	GAA Glu	GGA Gly	TTT Phe	GAT Asp	GCT Ala	TTG Leu	AGA Arg	2517
	225				230				235						240	

ATA	ACA	AAA	GAA	TTA	CTC	CAA	GAA	ATT	GGC	AAA	TTT	GAC	TCG	AAG	GAT	2565
Ile	Thr	Lys	Glu	Leu	Leu	Gln	Glu	Ile	Gly	Lys	Phe	Asp	Ser	Lys	Asp	
				245					250						255	
GTC	CAC	AAC	AAT	CTT	AAC	CAG	CTT	CAA	GTC	AAA	TTG	AAG	GAA	AGT	TTG	2613
Val	His	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Val	Lys	Leu	Lys	Glu	Ser	Leu	
			260					265					270			
AAG	GGA	AAG	AAG	TTC	CTT	ATT	GTT	TTG	GAT	GAT	GTG	TGG	AAT	GAA	AAT	2661
Lys	Gly	Lys	Lys	Phe	Leu	Ile	Val	Leu	Asp	Asp	Val	Trp	Asn	Glu	Asn	
		275					280					285				
TAC	AAC	GAG	TGG	AAT	GAC	TTG	AGA	AAT	ATT	TTT	GCA	CAA	GGA	GAT	ATA	2709
Tyr	Asn	Glu	Trp	Asn	Asp	Leu	Arg	Asn	Ile	Phe	Ala	Gln	Gly	Asp	Ile	
	290					295					300					
GGA	AGT	AAG	ATC	ATT	GTG	ACG	ACA	CGC	AAA	GAC	AGT	GTT	GCC	TTG	ATG	2757
Gly	Ser	Lys	Ile	Ile	Val	Thr	Thr	Arg	Lys	Asp	Ser	Val	Ala	Leu	Met	
305					310					315					320	
ATG	GGA	AAT	GAG	CAA	ATT	CGC	ATG	GGC	AAT	TTG	TCT	ACC	GAA	GCC	TCT	2805
Met	Gly	Asn	Glu	Gln	Ile	Arg	Met	Gly	Asn	Leu	Ser	Thr	Glu	Ala	Ser	
				325					330					335		
TGG	TCT	TTA	TTT	CAA	AGA	CAT	GCA	TTT	GAA	AAC	ATG	GAT	CCT	ATG	GGA	2853
Trp	Ser	Leu	Phe	Gln	Arg	His	Ala	Phe	Glu	Asn	Met	Asp	Pro	Met	Gly	
			340					345					350			
CAT	CCG	GAA	CTT	GAA	GAG	GTC	GGA	AGA	CAA	ATT	GCA	GCC	AAG	TGC	AAA	2901
His	Pro	Glu	Leu	Glu	Glu	Val	Gly	Arg	Gln	Ile	Ala	Ala	Lys	Cys	Lys	
		355					360					365				
GGA	CTG	CCC	TTA	GCT	CTG	AAG	ACG	CTC	GCT	GGC	ATG	TTA	CGC	TCC	AAA	2949
Gly	Leu	Pro	Leu	Ala	Leu	Lys	Thr	Leu	Ala	Gly	Met	Leu	Arg	Ser	Lys	
	370					375					380					
TCA	GAG	GTT	GAA	GAG	TGG	AAA	CGT	ATT	TTG	AGA	AGT	GAA	ATA	TGG	GAG	2997
Ser	Glu	Val	Glu	Glu	Trp	Lys	Arg	Ile	Leu	Arg	Ser	Glu	Ile	Trp	Glu	
385					390					395					400	
CTG	CCA	CAC	AAT	GAC	ATA	TTA	CCA	GCG	TTG	ATG	TTG	AGC	TAC	AAT	GAT	3045
Leu	Pro	His	Asn	Asp	Ile	Leu	Pro	Ala	Leu	Met	Leu	Ser	Tyr	Asn	Asp	
				405					410					415		
CTT	CCC	GCA	CAT	TTA	AAG	CGA	TGC	TTT	TCT	TTT	TGT	GCA	ATA	TTT	CCT	3093
Leu	Pro	Ala	His	Leu	Lys	Arg	Cys	Phe	Ser	Phe	Cys	Ala	Ile	Phe	Pro	
			420					425					430			
AAA	GAT	TAT	CCA	TTT	AGG	AAA	GAA	CAA	GTT	ATT	CAT	CTA	TGG	ATT	GCC	3141
Lys	Asp	Tyr	Pro	Phe	Arg	Lys	Glu	Gln	Val	Ile	His	Leu	Trp	Ile	Ala	
		435					440					445				
AAT	GGT	CTC	GTA	CCA	GTG	AAA	GAT	GAA	ATA	AAT	CAA	GAT	TTA	GGC	AAC	3189
Asn	Gly	Leu	Val	Pro	Val	Lys	Asp	Glu	Ile	Asn	Gln	Asp	Leu	Gly	Asn	
	450					455					460					
CAA	TAC	TTT	CTA	GAG	TTG	AGA	TCA	AGA	TCA	TTA	TTT	GAA	AAG	GTC	CCA	3237
Gln	Tyr	Phe	Leu	Glu	Leu	Arg	Ser	Arg	Ser	Leu	Phe	Glu	Lys	Val	Pro	
465					470					475					480	

AAT CCT TCT AAA AGG AAC ATA GAG GAA TTA TTC CTT ATG CAT GAC CTT	3285
Asn Pro Ser Lys Arg Asn Ile Glu Glu Leu Phe Leu Met His Asp Leu	
485 490 495	
GTC AAT GAT TTA GCC CAA CTT GCA TCT TCA AAA CTT TGT ATC AGG TTA	3333
Val Asn Asp Leu Ala Gln Leu Ala Ser Ser Lys Leu Cys Ile Arg Leu	
500 505 510	
GAA GAG AGC CAA GGA TCT CAT ATG TTG GAA CAA TGT CGG CAC TTA TCT	3381
Glu Glu Ser Gln Gly Ser His Met Leu Glu Gln Cys Arg His Leu Ser	
515 520 525	
TAT TCA ATA GGA TTT AAT GGT GAG TTT AAG AAA TTG ACA CCC CTC TAC	3429
Tyr Ser Ile Gly Phe Asn Gly Glu Phe Lys Lys Leu Thr Pro Leu Tyr	
530 535 540	
AAA TTG GAG CAG TTG AGG ACA TTG CTT CCG ATA CGT ATT GAA TTC AGA	3477
Lys Leu Glu Gln Leu Arg Thr Leu Leu Pro Ile Arg Ile Glu Phe Arg	
545 550 555 560	
TTG CAC AAT CTA AGC AAG AGG GTG TTG CAT AAC ATA CTG CCT ACA CTA	3525
Leu His Asn Leu Ser Lys Arg Val Leu His Asn Ile Leu Pro Thr Leu	
565 570 575	
AGA TCC TTG AGG GCC CTA TCA TTC TCT CAA TAC AAG ATT AAG GAG TTG	3573
Arg Ser Leu Arg Ala Leu Ser Phe Ser Gln Tyr Lys Ile Lys Glu Leu	
580 585 590	
CCA AAT GAC TTG TTT ACC AAA TTA AAG CTC CTC AGA TTT TTG GAT ATT	3621
Pro Asn Asp Leu Phe Thr Lys Leu Lys Leu Leu Arg Phe Leu Asp Ile	
595 600 605	
TCT CGG ACA TGG ATT ACA AAG TTG CCG GAT TCC ATT TGT GGA TTA TAT	3669
Ser Arg Thr Trp Ile Thr Lys Leu Pro Asp Ser Ile Cys Gly Leu Tyr	
610 615 620	
AAC TTG GAG ACA CTT CTC CTG TCA TCT TGT GCT GAT CTT GAG GAG CTA	3717
Asn Leu Glu Thr Leu Leu Leu Ser Ser Cys Ala Asp Leu Glu Glu Leu	
625 630 635 640	
CCG CTG CAG ATG GAG AAG TTG ATT AAC TTG CGT CAT CTT GAC GTA AGC	3765
Pro Leu Gln Met Glu Lys Leu Ile Asn Leu Arg His Leu Asp Val Ser	
645 650 655	
AAC ACT CGG CGC TTG AAG ATG CCA CTA CAT CTG AGC AGG TTG AAA AGC	3813
Asn Thr Arg Arg Leu Lys Met Pro Leu His Leu Ser Arg Leu Lys Ser	
660 665 670	
CTC CAA GTG TTG GTG GGA CCC AAG TTT TTT GTA GAT GGT TGG AGA ATG	3861
Leu Gln Val Leu Val Gly Pro Lys Phe Phe Val Asp Gly Trp Arg Met	
675 680 685	
GAA GAT TTG GGT GAA GCA CAA AAC TTA CAT GGA TCT CTA TCA GTT GTG	3909
Glu Asp Leu Gly Glu Ala Gln Asn Leu His Gly Ser Leu Ser Val Val	
690 695 700	
AAG TTG GAA AAT GTG GTT GAT AGA AGG GAA GCT GTG AAG GCA AAG ATG	3957
Lys Leu Glu Asn Val Val Asp Arg Arg Glu Ala Val Lys Ala Lys Met	
705 710 715 720	



AGG	GAG	AAG	AAT	CAT	GTT	GAG	CAA	TTA	TCA	TTG	GAG	TGG	AGT	GAA	AGT	4005
Arg	Glu	Lys	Asn	His	Val	Glu	Gln	Leu	Ser	Leu	Glu	Trp	Ser	Glu	Ser	
				725					730					735		
AGT	ATT	GCC	GAC	AAT	TCA	CAA	ACA	GAA	AGT	GAC	ATA	CTT	GAT	GAG	CTA	4053
Ser	Ile	Ala	Asp	Asn	Ser	Gln	Thr	Glu	Ser	Asp	Ile	Leu	Asp	Glu	Leu	
			740					745					750			
TGC	CCA	CAT	AAA	AAC	ATC	AAA	AAA	GTC	GAA	ATC	AGT	GGA	TAT	AGA	GGG	4101
Cys	Pro	His	Lys	Asn	Ile	Lys	Lys	Val	Glu	Ile	Ser	Gly	Tyr	Arg	Gly	
			755				760					765				
ACA	AAC	TTT	CCC	AAT	TGG	GTA	GCT	GAT	CCT	TTG	TTT	CTT	AAG	CTG	GTG	4149
Thr	Asn	Phe	Pro	Asn	Trp	Val	Ala	Asp	Pro	Leu	Phe	Leu	Lys	Leu	Val	
	770					775					780					
AAT	TTG	TCT	CTA	AGA	AAC	TGC	AAG	GAC	TGT	TAC	TCC	TTG	CCA	GCA	CTA	4197
Asn	Leu	Ser	Leu	Arg	Asn	Cys	Lys	Asp	Cys	Tyr	Ser	Leu	Pro	Ala	Leu	
	785				790				795						800	
GGA	CAA	CTC	CCT	TGT	TTG	AAA	TTC	CTT	TCC	GTT	AAA	GGG	ATG	CAT	GGA	4245
Gly	Gln	Leu	Pro	Cys	Leu	Lys	Phe	Leu	Ser	Val	Lys	Gly	Met	His	Gly	
				805					810					815		
ATA	AGA	GTG	GTG	ACG	GAA	GAA	TTC	TAT	GGC	AGA	TTG	TCC	TCC	AAA	AAG	4293
Ile	Arg	Val	Val	Thr	Glu	Glu	Phe	Tyr	Gly	Arg	Leu	Ser	Ser	Lys	Lys	
			820					825					830			
CCT	TTT	AAC	TCT	CTA	GAG	AAG	CTT	GAA	TTT	GAA	GAT	ATG	ACG	GAG	TGG	4341
Pro	Phe	Asn	Ser	Leu	Glu	Lys	Leu	Glu	Phe	Glu	Asp	Met	Thr	Glu	Trp	
		835					840					845				
AAG	CAA	TGG	CAC	GCA	CTA	GGA	ATT	GGA	GAG	TTC	CCT	ACA	CTT	GAG	AAC	4389
Lys	Gln	Trp	His	Ala	Leu	Gly	Ile	Gly	Glu	Phe	Pro	Thr	Leu	Glu	Asn	
	850					855					860					
CTT	TCA	ATT	AAA	AAT	TGC	CCT	GAG	CTC	AGT	TTG	GAG	ATA	CCC	ATC	CAA	4437
Leu	Ser	Ile	Lys	Asn	Cys	Pro	Glu	Leu	Ser	Leu	Glu	Ile	Pro	Ile	Gln	
					870					875					880	
TTT	TCA	AGT	TTA	AAA	AGG	TTA	GAA	GTT	AGT	GAT	TGT	CCA	GTT	GTT	TTT	4485
Phe	Ser	Ser	Leu	Lys	Arg	Leu	Glu	Val	Ser	Asp	Cys	Pro	Val	Val	Phe	
				885					890					895		
GAT	GAT	GCC	CAA	CTG	TTT	AGA	TCC	CAA	CTT	GAG	GCA	ATG	AAG	CAG	ATT	4533
Asp	Asp	Ala	Gln	Leu	Phe	Arg	Ser	Gln	Leu	Glu	Ala	Met	Lys	Gln	Ile	
			900					905					910			
GAG	GAA	ATA	GAT	ATA	TGT	GAT	TGT	AAC	TCT	GTT	ACC	TCC	TTT	CCT	TTT	4581
Glu	Glu	Ile	Asp	Ile	Cys	Asp	Cys	Asn	Ser	Val	Thr	Ser	Phe	Pro	Phe	
			915				920					925				
AGC	ATA	CTG	CCA	ACT	ACC	TTG	AAG	AGA	ATA	CAG	ATA	TCT	CGT	TGC	CCA	4629
Ser	Ile	Leu	Pro	Thr	Thr	Leu	Lys	Arg	Ile	Gln	Ile	Ser	Arg	Cys	Pro	
	930					935					940					
AAA	TTG	AAA	TTG	GAG	GCG	CCA	GTT	GGT	GAG	ATG	TTT	GTG	GAG	TAT	TTG	4677
Lys	Leu	Lys	Leu	Glu	Ala	Pro	Val	Gly	Glu	Met	Phe	Val	Glu	Tyr	Leu	
	945				950				955						960	

AGA GTG AAT GAT TGT GGT TGT GTA GAT GAT ATA TCA CCT GAG TTT CTC	4725
Arg Val Asn Asp Cys Gly Cys Val Asp Asp Ile Ser Pro Glu Phe Leu	
965 970 975	
CCA ACA GCA CGT CAA TTG AGT ATT GAA AAT TGC CAG AAC GTT ACT AGG	4773
Pro Thr Ala Arg Gln Leu Ser Ile Glu Asn Cys Gln Asn Val Thr Arg	
980 985 990	
TTT TTG ATT CCT ACT GCC ACT GAA ACT CTC CGT ATT TCG AAT TGT GAG	4821
Phe Leu Ile Pro Thr Ala Thr Glu Thr Leu Arg Ile Ser Asn Cys Glu	
995 1000 1005	
AAT GTT GAA AAA CTA TCG GTG GCA TGT GGA GGA GCG GCC CAG ATG ACG	4869
Asn Val Glu Lys Leu Ser Val Ala Cys Gly Gly Ala Ala Gln Met Thr	
1010 1015 1020	
TCA CTG AAT ATT TGG GGA TGT AAG AAG CTC AAG TGT CTT CCA GAA CTC	4917
Ser Leu Asn Ile Trp Gly Cys Lys Lys Leu Lys Cys Leu Pro Glu Leu	
1025 1030 1035 1040	
CTT CCA TCT CTC AAG GAA CTG CGT CTG TCT GAT TGT CCA GAA ATA GAA	4965
Leu Pro Ser Leu Lys Glu Leu Arg Leu Ser Asp Cys Pro Glu Ile Glu	
1045 1050 1055	
GGA GAA TTG CCC TTC AAT TTA GAA ATA CTC CGT ATC ATA TAT TGC AAG	5013
Gly Glu Leu Pro Phe Asn Leu Glu Ile Leu Arg Ile Ile Tyr Cys Lys	
1060 1065 1070	
AAA CTG GTG AAT GGC CGA AAG GAG TGG CAT TTA CAG AGA CTC ACA GAG	5061
Lys Leu Val Asn Gly Arg Lys Glu Trp His Leu Gln Arg Leu Thr Glu	
1075 1080 1085	
TTA TGG ATC GAT CAT GAT GGG AGT GAC GAA GAT ATT GAA CAT TGG GAG	5109
Leu Trp Ile Asp His Asp Gly Ser Asp Glu Asp Ile Glu His Trp Glu	
1090 1095 1100	
TTG CCT TGT TCT ATT CAG AGA CTT ACC ATA AAG AAT CTT AAA ACA TTA	5157
Leu Pro Cys Ser Ile Gln Arg Leu Thr Ile Lys Asn Leu Lys Thr Leu	
1105 1110 1115 1120	
AGC AGC CAA CAT CTC AAA AGC CTC ACC TCT CTT CAA TAT CTA TGT ATT	5205
Ser Ser Gln His Leu Lys Ser Leu Thr Ser Leu Gln Tyr Leu Cys Ile	
1125 1130 1135	
GAG GGT TAT TTA TCT CAG ATT CAG TCA CAA GGC CAG CTT TCC TCC TTT	5253
Glu Gly Tyr Leu Ser Gln Ile Gln Ser Gln Gly Gln Leu Ser Ser Phe	
1140 1145 1150	
TCT CAC CTC ACT TCG CTT CAA ACT CTA CAA ATC TGG AAT TTC CTT AAT	5301
Ser His Leu Thr Ser Leu Gln Thr Leu Gln Ile Trp Asn Phe Leu Asn	
1155 1160 1165	
CTC CAA TCA CTT GCT GAA TCA GCA CTG CCC TCC TCC CTC TCT CAC CTG	5349
Leu Gln Ser Leu Ala Glu Ser Ala Leu Pro Ser Ser Leu Ser His Leu	
1170 1175 1180	
GAG ATA GAT GAT TGC CCT AAT CTC CAA TCA CTC TTC GAA TCA GCA CTG	5397
Glu Ile Asp Asp Cys Pro Asn Leu Gln Ser Leu Phe Glu Ser Ala Leu	
1185 1190 1195 1200	

CCC TCC TCC CTC TCT CAG CTG TTC ATC CAG GAT TGC CCT AAT CTC CAA	5445
Pro Ser Ser Leu Ser Gln Leu Phe Ile Gln Asp Cys Pro Asn Leu Gln	
1205 1210 1215	
TCC CTT CCA TTT AAA GGG ATG CCC TCT TCC CTC TCT AAA CTA TCT ATT	5493
Ser Leu Pro Phe Lys Gly Met Pro Ser Ser Leu Ser Lys Leu Ser Ile	
1220 1225 1230	
TTC AAT TGC CCA TTG CTC ACA CCA CTA CTA GAA TTT GAC AAG GGG GAA	5541
Phe Asn Cys Pro Leu Leu Thr Pro Leu Leu Glu Phe Asp Lys Gly Glu	
1235 1240 1245	
TAC TGG CCA CAA ATT GCT CAT ATT CCC ATC ATA AAT ATC GAT TGG AAA	5589
Tyr Trp Pro Gln Ile Ala His Ile Pro Ile Ile Asn Ile Asp Trp Lys	
1250 1255 1260	
TAT ATT TAACAATTAA AACAAATGGC TCTCCAATG ATGTAAGCTA TTCGTTACCC	5645
Tyr Ile	
1265	
TTAGAAGCTT TTTATGATTC TATGTTTCTC ATTGCTTATT GGTTCATGCT CTTACCGTGT	5705
TTTAATTCAC GTCTCAATTG CCACCATGTT TAATCGAAAG TTTTGTAGTTC TTGTAATCAT	5765
CAACCATCCT ATGTCACCTAG AAATTTTGAT AGGTAAAAGA GGTAGACAAA AAAGCTAAAC	5825
ATCTTTTTTTC TTTTCGTATAG CGACCAAACA ACTACATTTT GATAGGTAAG GGCTATAGAT	5885
ATACATTTGTC AGGGTGTTAA ACCAAGGAGT AAGAAAATCA CTGTCTTCAG ATATCTTCTC	5945
TTGCATATAC TTTTGCAATT TTAAGCTACA TTTTGAAGCTC ATGTGTTGTT GCTAACTTAA	6005
ACATGTTTTG TGCTTAATCA GATGTGGATT TTGAAGAGCG AGTACGACAA GTCTGGTACA	6065
TTAATTGTCC GTAGAAGTGT TTCTAAGGTG CTGCTGCTAT TTTTACATCT GTTCCCGAGT	6125
TTTGTTTTTT TTTTAAATCT TTCCACTAAA GCTATTATGT CGTCCACAGT GAATTTTCAG	6185
GTCTGTTGTT ATAGGCAAGT CTTTGAGATG CGACTATCAA AGAAGGGCGA TTACAATCAG	6245
TGTACCGCTG AAATATTTT ATGTTTCCAG TGCAAGCCTC TTTTGTAAGT TGACAACTC	6305
GATTAGTTAA TATGTTTGGG ACTCAACTAG TGGTTAGAGT ACTCATTTTG TAAGACTTGT	6365
GTACAGAAAA TCAAATTAGA ATTATAACTC GTGATGGTTG AATAAACTCT AAGAAGTACT	6425
GATATATTTT TTAGTGGATA TGTTGTTTGC TCATTGCGTG TTTGATATCC ACATTGGAGT	6485
CCAACTAAAT TCGAATTTGC ACAATCGAAG GAGCGGTGCT CCTGGCATGA TTTTTTCCC	6545
ATTCTACGAC TAGTGCTCCT AAATCTAAT TAAGCATAGA AAAATCTCAA CTATCTCACC	6605
CAACTCATAT CAGGATAGAG TATTCCCTGA GGAGGATTCC TTCAGTTACA AAA	6658

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1266 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Met Glu Ile Gly Leu Ala Val Gly Gly Ala Phe Leu Ser Ser Ala Leu
 1           5           10           15
Asn Val Leu Phe Asp Arg Leu Ala Pro Asn Gly Asp Leu Leu Asn Met
          20           25           30
Phe Arg Lys His Lys Asp His Val Lys Leu Leu Lys Lys Leu Lys Met
          35           40           45
Thr Leu Arg Gly Ile Gln Ile Val Leu Ser Asp Ala Glu Asn Lys Gln
          50           55           60
Ala Ser Asn Pro Ser Val Arg Asp Trp Leu Asn Glu Leu Arg Asp Ala
          65           70           75           80
Val Asp Ser Ala Glu Asn Leu Ile Glu Glu Val Asn Tyr Glu Ala Leu
          85           90           95
Arg Leu Lys Val Glu Gly Gln His Gln Asn Phe Ser Glu Thr Ser Asn
          100          105          110
Gln Gln Val Ser Asp Asp Phe Phe Leu Asn Ile Lys Asp Lys Leu Glu
          115          120          125
Asp Thr Ile Glu Thr Leu Lys Asp Leu Gln Glu Gln Ile Gly Leu Leu
          130          135          140
Gly Leu Lys Glu Tyr Phe Asp Ser Thr Lys Leu Glu Thr Arg Arg Pro
          145          150          155          160
Ser Thr Ser Val Asp Asp Glu Ser Asp Ile Phe Gly Arg Gln Ser Glu
          165          170          175
Ile Glu Asp Leu Ile Asp Arg Leu Leu Ser Glu Gly Ala Ser Gly Lys
          180          185          190
Lys Leu Thr Val Val Pro Ile Val Gly Met Gly Gly Gln Gly Lys Thr
          195          200          205
Thr Leu Ala Lys Ala Val Tyr Asn Asp Glu Arg Val Lys Asn His Phe
          210          215          220
Asp Leu Lys Ala Trp Tyr Cys Val Ser Glu Gly Phe Asp Ala Leu Arg
          225          230          235          240
Ile Thr Lys Glu Leu Leu Gln Glu Ile Gly Lys Phe Asp Ser Lys Asp
          245          250          255
Val His Asn Asn Leu Asn Gln Leu Gln Val Lys Leu Lys Glu Ser Leu
          260          265          270
Lys Gly Lys Lys Phe Leu Ile Val Leu Asp Asp Val Trp Asn Glu Asn
          275          280          285
Tyr Asn Glu Trp Asn Asp Leu Arg Asn Ile Phe Ala Gln Gly Asp Ile
          290          295          300

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Gly	Ser	Lys	Ile	Ile	Val	Thr	Thr	Arg	Lys	Asp	Ser	Val	Ala	Leu	Met	
305					310					315					320	
Met	Gly	Asn	Glu	Gln	Ile	Arg	Met	Gly	Asn	Leu	Ser	Thr	Glu	Ala	Ser	
				325					330					335		
Trp	Ser	Leu	Phe	Gln	Arg	His	Ala	Phe	Glu	Asn	Met	Asp	Pro	Met	Gly	
			340					345					350			
His	Pro	Glu	Leu	Glu	Glu	Val	Gly	Arg	Gln	Ile	Ala	Ala	Lys	Cys	Lys	
		355					360					365				
Gly	Leu	Pro	Leu	Ala	Leu	Lys	Thr	Leu	Ala	Gly	Met	Leu	Arg	Ser	Lys	
	370					375					380					
Ser	Glu	Val	Glu	Glu	Trp	Lys	Arg	Ile	Leu	Arg	Ser	Glu	Ile	Trp	Glu	
385					390					395					400	
Leu	Pro	His	Asn	Asp	Ile	Leu	Pro	Ala	Leu	Met	Leu	Ser	Tyr	Asn	Asp	
			405						410					415		
Leu	Pro	Ala	His	Leu	Lys	Arg	Cys	Phe	Ser	Phe	Cys	Ala	Ile	Phe	Pro	
		420						425					430			
Lys	Asp	Tyr	Pro	Phe	Arg	Lys	Glu	Gln	Val	Ile	His	Leu	Trp	Ile	Ala	
	435						440					445				
Asn	Gly	Leu	Val	Pro	Val	Lys	Asp	Glu	Ile	Asn	Gln	Asp	Leu	Gly	Asn	
	450					455					460					
Gln	Tyr	Phe	Leu	Glu	Leu	Arg	Ser	Arg	Ser	Leu	Phe	Glu	Lys	Val	Pro	
465					470					475					480	
Asn	Pro	Ser	Lys	Arg	Asn	Ile	Glu	Glu	Leu	Phe	Leu	Met	His	Asp	Leu	
			485						490					495		
Val	Asn	Asp	Leu	Ala	Gln	Leu	Ala	Ser	Ser	Lys	Leu	Cys	Ile	Arg	Leu	
		500						505					510			
Glu	Glu	Ser	Gln	Gly	Ser	His	Met	Leu	Glu	Gln	Cys	Arg	His	Leu	Ser	
	515						520					525				
Tyr	Ser	Ile	Gly	Phe	Asn	Gly	Glu	Phe	Lys	Lys	Leu	Thr	Pro	Leu	Tyr	
	530					535					540					
Lys	Leu	Glu	Gln	Leu	Arg	Thr	Leu	Leu	Pro	Ile	Arg	Ile	Glu	Phe	Arg	
545					550					555					560	
Leu	His	Asn	Leu	Ser	Lys	Arg	Val	Leu	His	Asn	Ile	Leu	Pro	Thr	Leu	
			565						570					575		
Arg	Ser	Leu	Arg	Ala	Leu	Ser	Phe	Ser	Gln	Tyr	Lys	Ile	Lys	Glu	Leu	
		580						585					590			
Pro	Asn	Asp	Leu	Phe	Thr	Lys	Leu	Lys	Leu	Leu	Arg	Phe	Leu	Asp	Ile	
		595					600					605				
Ser	Arg	Thr	Trp	Ile	Thr	Lys	Leu	Pro	Asp	Ser	Ile	Cys	Gly	Leu	Tyr	
	610					615					620					

Asn	Leu	Glu	Thr	Leu	Leu	Leu	Ser	Ser	Cys	Ala	Asp	Leu	Glu	Glu	Leu	625	630	635	640
Pro	Leu	Gln	Met	Glu	Lys	Leu	Ile	Asn	Leu	Arg	His	Leu	Asp	Val	Ser	645	650	655	
Asn	Thr	Arg	Arg	Leu	Lys	Met	Pro	Leu	His	Leu	Ser	Arg	Leu	Lys	Ser	660	665	670	
Leu	Gln	Val	Leu	Val	Gly	Pro	Lys	Phe	Phe	Val	Asp	Gly	Trp	Arg	Met	675	680	685	
Glu	Asp	Leu	Gly	Glu	Ala	Gln	Asn	Leu	His	Gly	Ser	Leu	Ser	Val	Val	690	695	700	
Lys	Leu	Glu	Asn	Val	Val	Asp	Arg	Arg	Glu	Ala	Val	Lys	Ala	Lys	Met	705	710	715	720
Arg	Glu	Lys	Asn	His	Val	Glu	Gln	Leu	Ser	Leu	Glu	Trp	Ser	Glu	Ser	725	730	735	
Ser	Ile	Ala	Asp	Asn	Ser	Gln	Thr	Glu	Ser	Asp	Ile	Leu	Asp	Glu	Leu	740	745	750	
Cys	Pro	His	Lys	Asn	Ile	Lys	Lys	Val	Glu	Ile	Ser	Gly	Tyr	Arg	Gly	755	760	765	
Thr	Asn	Phe	Pro	Asn	Trp	Val	Ala	Asp	Pro	Leu	Phe	Leu	Lys	Leu	Val	770	775	780	
Asn	Leu	Ser	Leu	Arg	Asn	Cys	Lys	Asp	Cys	Tyr	Ser	Leu	Pro	Ala	Leu	785	790	795	800
Gly	Gln	Leu	Pro	Cys	Leu	Lys	Phe	Leu	Ser	Val	Lys	Gly	Met	His	Gly	805	810	815	
Ile	Arg	Val	Val	Thr	Glu	Glu	Phe	Tyr	Gly	Arg	Leu	Ser	Ser	Lys	Lys	820	825	830	
Pro	Phe	Asn	Ser	Leu	Glu	Lys	Leu	Glu	Phe	Glu	Asp	Met	Thr	Glu	Trp	835	840	845	
Lys	Gln	Trp	His	Ala	Leu	Gly	Ile	Gly	Glu	Phe	Pro	Thr	Leu	Glu	Asn	850	855	860	
Leu	Ser	Ile	Lys	Asn	Cys	Pro	Glu	Leu	Ser	Leu	Glu	Ile	Pro	Ile	Gln	865	870	875	880
Phe	Ser	Ser	Leu	Lys	Arg	Leu	Glu	Val	Ser	Asp	Cys	Pro	Val	Val	Phe	885	890	895	
Asp	Asp	Ala	Gln	Leu	Phe	Arg	Ser	Gln	Leu	Glu	Ala	Met	Lys	Gln	Ile	900	905	910	
Glu	Glu	Ile	Asp	Ile	Cys	Asp	Cys	Asn	Ser	Val	Thr	Ser	Phe	Pro	Phe	915	920	925	
Ser	Ile	Leu	Pro	Thr	Thr	Leu	Lys	Arg	Ile	Gln	Ile	Ser	Arg	Cys	Pro	930	935	940	

Lys	Leu	Lys	Leu	Glu	Ala	Pro	Val	Gly	Glu	Met	Phe	Val	Glu	Tyr	Leu	945	950	955	960
Arg	Val	Asn	Asp	Cys	Gly	Cys	Val	Asp	Asp	Ile	Ser	Pro	Glu	Phe	Leu	965	970	975	
Pro	Thr	Ala	Arg	Gln	Leu	Ser	Ile	Glu	Asn	Cys	Gln	Asn	Val	Thr	Arg	980	985	990	
Phe	Leu	Ile	Pro	Thr	Ala	Thr	Glu	Thr	Leu	Arg	Ile	Ser	Asn	Cys	Glu	995	1000	1005	
Asn	Val	Glu	Lys	Leu	Ser	Val	Ala	Cys	Gly	Gly	Ala	Ala	Gln	Met	Thr	1010	1015	1020	
Ser	Leu	Asn	Ile	Trp	Gly	Cys	Lys	Lys	Leu	Lys	Cys	Leu	Pro	Glu	Leu	1025	1030	1035	1040
Leu	Pro	Ser	Leu	Lys	Glu	Leu	Arg	Leu	Ser	Asp	Cys	Pro	Glu	Ile	Glu	1045	1050	1055	
Gly	Glu	Leu	Pro	Phe	Asn	Leu	Glu	Ile	Leu	Arg	Ile	Ile	Tyr	Cys	Lys	1060	1065	1070	
Lys	Leu	Val	Asn	Gly	Arg	Lys	Glu	Trp	His	Leu	Gln	Arg	Leu	Thr	Glu	1075	1080	1085	
Leu	Trp	Ile	Asp	His	Asp	Gly	Ser	Asp	Glu	Asp	Ile	Glu	His	Trp	Glu	1090	1095	1100	
Leu	Pro	Cys	Ser	Ile	Gln	Arg	Leu	Thr	Ile	Lys	Asn	Leu	Lys	Thr	Leu	1105	1110	1115	1120
Ser	Ser	Gln	His	Leu	Lys	Ser	Leu	Thr	Ser	Leu	Gln	Tyr	Leu	Cys	Ile	1125	1130	1135	
Glu	Gly	Tyr	Leu	Ser	Gln	Ile	Gln	Ser	Gln	Gly	Gln	Leu	Ser	Ser	Phe	1140	1145	1150	
Ser	His	Leu	Thr	Ser	Leu	Gln	Thr	Leu	Gln	Ile	Trp	Asn	Phe	Leu	Asn	1155	1160	1165	
Leu	Gln	Ser	Leu	Ala	Glu	Ser	Ala	Leu	Pro	Ser	Ser	Leu	Ser	His	Leu	1170	1175	1180	
Glu	Ile	Asp	Asp	Cys	Pro	Asn	Leu	Gln	Ser	Leu	Phe	Glu	Ser	Ala	Leu	1185	1190	1195	1200
Pro	Ser	Ser	Leu	Ser	Gln	Leu	Phe	Ile	Gln	Asp	Cys	Pro	Asn	Leu	Gln	1205	1210	1215	
Ser	Leu	Pro	Phe	Lys	Gly	Met	Pro	Ser	Ser	Leu	Ser	Lys	Leu	Ser	Ile	1220	1225	1230	
Phe	Asn	Cys	Pro	Leu	Leu	Thr	Pro	Leu	Leu	Glu	Phe	Asp	Lys	Gly	Glu	1235	1240	1245	

Tyr Trp Pro Gln Ile Ala His Ile Pro Ile Ile Asn Ile Asp Trp Lys  
1250 1255 1260

Tyr Ile  
1265